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# SEQUENCE LISTING

<110> FUJIREBIO INC.

<120> Anti-SARS virus antibody, hybridoma producing the same and immunoassay reagent including the same

<130> 04PF0289-PCT

<150> JP 2003-373779

<151> 2003-10-31

<150> JP 2004-034268

<151> 2004-02-10

<160> 3

<170> PatentIn version 3.1

<210> 1

<211> 1269

<212> DNA

<213> Coronavirus

<220>

<221> CDS

<222> (1).. (1269)

<223>

<400> 1

atg tct gat aat gga ccc caa tca aac caa cgt agt gcc ccc cgc att	48
Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile	
1                    5                    10                    15	

aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat gga gga	96
Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly	
20                    25                    30	

cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta ccc aat	144
Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn	
35                    40                    45	

aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag gag gaa	192
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu	
50                    55                    60	

ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat agt ggt	240
Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly	

65	70	75	80	
cca gat gac caa att ggc tac tac cga aga gct acc cga cga gtt cgt				288
Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg				
	85	90	95	
ggg ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac ttc tat				336
Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr				
	100	105	110	
tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct aac aaa				384
Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys				
	115	120	125	
gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca ccc aaa				432
Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys				
	130	135	140	
gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc gtg cta				480
Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu				
	145	150	155	160
caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca gag gga				528
Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly				
	165	170	175	
agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt agt cgc				576
Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg				
	180	185	190	
ggg aat tca aga aat tca act cct ggc agc agt agg gga aat tct cct				624
Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro				
	195	200	205	
gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta ttg ctg				672
Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu				
	210	215	220	
cta gac aga ttg aac cag ctt gag agc aaa gtt tct ggt aaa ggc caa				720
Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln				
	225	230	235	240
caa caa caa ggc caa act gtc act aag aaa tct gct gct gag gca tct				768
Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser				
	245	250	255	
aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac gtc act				816
Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr				

260	265	270	
caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat ttc ggg Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly 275 280 285			864
gac caa gac cta atc aga caa gga act gat tac aaa cat tgg ccg caa Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln 290 295 300			912
att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg tca cgc Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg 305 310 315 320			960
att ggc atg gaa gtc aca cct tcg gga aca tgg ctg act tat cat gga Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly 325 330 335			1008
gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac gtc ata Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile 340 345 350			1056
ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca aca gag Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu 355 360 365			1104
cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct ttg ccg Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro 370 375 380			1152
cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg gct gac Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp 385 390 395 400			1200
atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga gct tct Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser 405 410 415			1248
gct gat tca act cag gca taa Ala Asp Ser Thr Gln Ala 420			1269

<210> 2  
 <211> 422  
 <212> PRT  
 <213> Coronavirus

&lt;400&gt; 2

Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile  
 1 5 10 15

Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly  
 20 25 30

Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn  
 35 40 45

Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu  
 50 55 60

Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly  
 65 70 75 80

Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg  
 85 90 95

Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr  
 100 105 110

Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys  
 115 120 125

Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys  
 130 135 140

Asp His Ile Gly Thr Arg Asn Pro Asn Asn Ala Ala Thr Val Leu  
 145 150 155 160

Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly  
 165 170 175

Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg  
 180 185 190

Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro  
 195 200 205

Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu  
 210 215 220

Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln  
 225 230 235 240

Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser  
 245 250 255

Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr  
 260 265 270

Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly  
 275 280 285

Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln  
 290 295 300

Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg  
 305 310 315 320

Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly  
 325 330 335

Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile  
 340 345 350

Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu  
 355 360 365

Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro  
 370 375 380

Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp  
 385 390 395 400

Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser  
 405 410 415

Ala Asp Ser Thr Gln Ala  
 420

<210> 3  
 <211> 18  
 <212> PRT  
 <213> Artificial

<220>

<223> A peptide sequence consisting of the amino acids 244-260 of SEQ I  
 D NO:2 and Cysteine

<400> 3

Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser Lys Lys Pro  
 1 5 10 15

Arg Cys